Database :   A_Geneseq_16Dec04:*
                  1: geneseqp1980s:*
                  2: geneseqp1990s:*
                  3: geneseqp2000s:*
                  4: geneseqp2001s:*
                  5: geneseqp2002s:*
                  6: geneseqp2003as:*
                  7: geneseqp2003bs:*
                  8: geneseqp2004s:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                              SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2619	100.0	514	7	ADG63312	Adg63312 Human IMP
2	2609	99.6	514	7	ADG63349	Adg63349 Human IMP
3	2605	99.5	514	2	AAR05432	Aar05432 Human IMP
4	2605	99.5	514	5	AAE18189	Aae18189 Human wil
5	2605	99.5	514	7	ADG63310	Adg63310 Human wil
6	2605	99.5	514	7	ADJ68634	Adj68634 Human hea
7	2605	99.5	514	8	ADO19228	Ado19228 Human PRO
8	2605	99.5	529	8	ADR66377	Adr66377 Human pro
9	2605	99.5	529	8	ADR66719	Adr66719 Human pro
10	2601	99.3	514	7	ADG63316	Adg63316 Human IMP
11	2601	99.3	514	7	ADG63314	Adg63314 Human IMP
12	2597	99.2	514	7	ADG63318	Adg63318 Human IMP
13	2595	99.1	514	5	AAU10695	Aau10695 Reference
14	2595	99.1	514	5	AAE18186	Aae18186 Human wil
15	2595	99.1	514	8	ADS88152	Ads88152 Human pro
16	2590	98.9	514	7	ADG63320	Adg63320 Human IMP
17	2569	98.1	514	7	ADG63340	Adg63340 Mouse IMP
18	2559	97.7	514	2	AAR05431	Aar05431 Chinese h
19	2555	97.6	514	7	ADG63338	Adg63338 Mouse wil
20	2234	85.3	514	5	AAE18188	Aae18188 Human wil
21	2234	85.3	514	5	ADI17228	Adi17228 Human NOV
22	2234	85.3	563	6	ADA54125	Ada54125 Human pro
23	2229	85.1	514	5	AAE18257	Aae18257 Human typ

RESULT 3
AAR05432

    Query Match   99.5%; Score 2605; DB 2; Length 514;
    Best Local Similarity   99.6%; Pred. No. 7.9e-246;
    Matches 512; Conservative   0; Mismatches   2; Indels   0; Gaps   0;

Qy   1 MADYLISGGTSYVPDDGLTAQQLFNCGDGLTYNDFLILPGYIDFTADQVDLTSALTKKIT 60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MADYLISGGTSYVPDDGLTAQQLFNCGDGLTYNDFLILPGYIDFTADQVDLTSALTKKIT 60

Qy   61 LKTPLVSSPMDTVTEAGMAIAMALTGGIGFIHHNCTPEFQANEVRKVKKYEQGFITDPVV 120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 LKTPLVSSPMDTVTEAGMAIAMALTGGIGFIHHNCTPEFQANEVRKVKKYEQGFITDPVV 120

Qy   121 LSPKDRVRDVFEAKARHGFCGIPITDTGRMGSRLVGIISSRDIDFLKEEEHDCFLEEIMT 180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db   121 LSPKDRVRDVFEAKARHGFCGIPITDTGRMGSRLVGIISSRDIDFLKEEEHDCFLEEIMT 180

Qy   181 KREDLVVAPRSITLKEANEILQRSKKGKLPIVNEDDELVAIIARTDLKKNRDYPLASKDA 240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 KREDLVVAPRSITLKEANEILQRSKKGKLPIVNEDDELVAIIARTDLKKNRDYPLASKDA 240

Qy   241 KKQLLCGAAIGTHEDDKYRLDLLAQAGVDVVVLDSSQGNSIFQINMIKYIKDKYPNLQVI 300
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 KKQLLCGAAIGTHEDDKYRLDLLAQAGVDVVVLDSSQGNSIFQINMIKYIKDKYPNLQVI 300

Qy   301 GGNVVTAAQAKNLIDAGVDALRVGMGSGSICIIQEVLACGRPQATAVYKVYEYARRFGVP 360
         ||||||||||||||||||||||||||||||| ||||||||||||||||| |||||||||
Db   301 GGNVVTAAQAKNLIDAGVDALRVGMGSGSICITQEVLACGRPQATAVYKVSEYARRFGVP 360

Qy   361 VIADGGIQNVGHIAKALALGASTVMMGSLLAATTEAPGEYFFSDGIRLKKYRGMGSLDAM 420
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 VIADGGIQNVGHIAKALALGASTVMMGSLLAATTEAPGEYFFSDGIRLKKYRGMGSLDAM 420

Qy   421 DKHLSSQNRYFSEADKIKVAQGVSGAVQDKGSIHKFVPYLIAGIQHSCQDIGAKSLTQVR 480
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 DKHLSSQNRYFSEADKIKVAQGVSGAVQDKGSIHKFVPYLIAGIQHSCQDIGAKSLTQVR 480

Qy   481 AMMYSGELKFEKRTSSAQVEGGVHSLHSYEKRLF 514
         ||||||||||||||||||||||||||||||||||
Db   481 AMMYSGELKFEKRTSSAQVEGGVHSLHSYEKRLF 514

```
Database :            Published_Applications_AA:*
                      1:  /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
                      2:  /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
                      3:  /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
                      4:  /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
                      5:  /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
                      6:  /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
                      7:  /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
                      8:  /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
                      9:  /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
                      10:  /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
                      11:  /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
                      12:  /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
                      13:  /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
                      14:  /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
                      15:  /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
                      16:  /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*
                      17:  /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep:*
                      18:  /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
                      19:  /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep:*
                      20:  /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
                      21:  /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
                      22:  /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2619	100.0	514	10	US-09-846-637A-4	Sequence 4, Appli
2	2605	99.5	514	9	US-09-853-918-63	Sequence 63, Appl
3	2605	99.5	514	10	US-09-846-637A-2	Sequence 2, Appli
4	2605	99.5	514	16	US-10-408-765A-440	Sequence 440, App
5	2601	99.3	514	10	US-09-846-637A-6	Sequence 6, Appli
6	2601	99.3	514	10	US-09-846-637A-8	Sequence 8, Appli
7	2597	99.2	514	10	US-09-846-637A-10	Sequence 10, Appl
8	2595	99.1	514	9	US-09-853-918-49	Sequence 49, Appl
9	2590	98.9	514	10	US-09-846-637A-12	Sequence 12, Appl

Database :   Issued_Patents_AA:*
                    1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
                    2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
                    3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
                    4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
                    5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                    6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                                SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2605	99.5	514	3	US-08-925-230-7	Sequence 7, Appli
2	2605	99.5	514	4	US-09-712-372-7	Sequence 7, Appli
3	2595	99.1	514	4	US-09-538-092-913	Sequence 913, App
4	2595	99.1	607	4	US-09-949-016-11614	Sequence 11614, A
5	2559	97.7	514	3	US-08-925-230-8	Sequence 8, Appli
6	2559	97.7	514	4	US-09-712-372-8	Sequence 8, Appli
7	2222	84.8	514	4	US-09-538-092-973	Sequence 973, App
8	1607.5	61.4	523	4	US-09-538-092-584	Sequence 584, App
9	1210.5	46.2	371	3	US-09-212-247C-9	Sequence 9, Appli
10	906	34.6	510	4	US-09-134-000C-5141	Sequence 5141, Ap
11	885	33.8	495	4	US-09-107-532A-4081	Sequence 4081, Ap
12	865	33.0	488	4	US-09-710-279-2308	Sequence 2308, Ap
13	865	33.0	494	3	US-09-134-001C-5024	Sequence 5024, Ap
14	862.5	32.9	558	4	US-09-252-991A-18187	Sequence 18187, A
15	859.5	32.8	497	4	US-09-328-352-6297	Sequence 6297, Ap
16	819	31.3	510	4	US-09-489-039A-11778	Sequence 11778, A
17	816	31.2	487	4	US-09-809-665A-169	Sequence 169, App
18	811	31.0	487	4	US-09-809-665A-24	Sequence 24, Appl
19	807.5	30.8	492	4	US-09-583-110-4390	Sequence 4390, Ap

RESULT 1
US-08-925-230-7
; Sequence 7, Application US/08925230
; Patent No. 6147194
; GENERAL INFORMATION:
;   APPLICANT: Collart, Frank
;   APPLICANT: Huberman, Eliezer
;   TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO IMPDH
;   TITLE OF INVENTION: AND GMP PRODUCTION
;   NUMBER OF SEQUENCES: 8
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Arnold, White & Durkee
;   STREET: P.O. Box 4433
;   CITY: Houston
;   STATE: Texas
;   COUNTRY: USA
;   ZIP: 77210
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/925,230
;   FILING DATE: September 8, 1997
;   CLASSIFICATION: 536
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 5,665,583
;   FILING DATE: 12-AUG-1988
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Wilson, Mark B.
;   REGISTRATION NUMBER: 37,259
.;   REFERENCE/DOCKET NUMBER: ARCD:274
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (512) 418-3000
;   TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 7:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 514 amino acids
;   TYPE: amino acid
;   STRANDEDNESS:
;   TOPOLOGY: linear
US-08-925-230-7

    Query Match   99..5%; Score 2605; DB 3; Length 514;
    Best Local Similarity   99.6%;. Pred. No. 4.2e-250;
    Matches 512; Conservative   0; Mismatches   2; Indels   0; Gaps   0;

Qy   1 MADYLISGGTSYVPDDGLTAQQLFNCGDGLTYNDFLILPGYIDFTADQVDLTSALTKKIT 60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MADYLISGGTSYVPDDGLTAQQLFNCGDGLTYNDFLILPGYIDFTADQVDLTSALTKKIT 60

Qy   61 LKTPLVSSPMDTVTEAGMAIAMALTGGIGFIHHNCTPEFQANEVRKVKKYEQGFITDPVV 120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 LKTPLVSSPMDTVTEAGMAIAMALTGGIGFIHHNCTPEFQANEVRKVKKYEQGFITDPVV 120

Qy   121 LSPKDRVRDVFEAKARHGFCGIPITDTGRMGSRLVGIISSRDIDFLKEEEHDCFLEEIMT 180

```
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121  LSPKDRVRDVFEAKARHGFCGIPITDTGRMGSRLVGIISSRDIDFLKEEEHDCFLEEIMT 180

Qy    181  KREDLVVAPRSITLKEANEILQRSKKGKLPIVNEDDELVAIIARTDLKKNRDYPLASKDA 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181  KREDLVVAPRSITLKEANEILQRSKKGKLPIVNEDDELVAIIARTDLKKNRDYPLASKDA 240

Qy    241  KKQLLCGAAIGTHEDDKYRLDLLAQAGVDVVVLDSSQGNSIFQINMIKYIKDKYPNLQVI 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241  KKQLLCGAAIGTHEDDKYRLDLLAQAGVDVVVLDSSQGNSIFQINMIKYIKDKYPNLQVI 300

Qy    301  GGNVVTAAQAKNLIDAGVDALRVGMGSGSICIIQEVLACGRPQATAVYKVYEYARRFGVP 360
            |||||||||||||||||||||||||||||||||||  ||||||||||||||||  ||||||||
Db    301  GGNVVTAAQAKNLIDAGVDALRVGMGSGSICITQEVLACGRPQATAVYKVSEYARRFGVP 360

Qy    361  VIADGGIQNVGHIAKALALGASTVMMGSLLAATTEAPGEYFFSDGIRLKKYRGMGSLDAM 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361  VIADGGIQNVGHIAKALALGASTVMMGSLLAATTEAPGEYFFSDGIRLKKYRGMGSLDAM 420

Qy    421  DKHLSSQNRYFSEADKIKVAQGVSGAVQDKGSIHKFVPYLIAGIQHSCQDIGAKSLTQVR 480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421  DKHLSSQNRYFSEADKIKVAQGVSGAVQDKGSIHKFVPYLIAGIQHSCQDIGAKSLTQVR 480

Qy    481  AMMYSGELKFEKRTSSAQVEGGVHSLHSYEKRLF 514
            ||||||||||||||||||||||||||||||||||
Db    481  AMMYSGELKFEKRTSSAQVEGGVHSLHSYEKRLF 514
```

```
Database :        PIR_79:*
                  1:  pir1:*
                  2:  pir2:*
                  3:  pir3:*
                  4:  pir4:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                              SUMMARIES
              %
Result   Query
   No.   Score Match Length DB ID   Description
----
     1   2595   99.1   514 1   A31997   IMP dehydrogenase
     2   2559   97.7   514 1   B31997   IMP dehydrogenase
     3   2555   97.6   514 1   JT0565   IMP dehydrogenase
     4   2222   84.8   514 1   A35566   IMP dehydrogenase
     5 1764.5   67.4   537 1   S41064   IMP dehydrogenase
     6 1635.5   62.4   537 1   S59508   IMP dehydrogenase
     7 1610.5   61.5   524 1   S50890   IMP dehydrogenase
     8 1607.5   61.4   523 1   S59402   IMP dehydrogenase
     9 1589.5   60.7   523 1   S48997   IMP dehydrogenase
    10 1473.5   56.3   524 1   T40127   IMP dehydrogenase
    11 1385.5   52.9   512 1   A55407   IMP dehydrogenase
    12 1363.5   52.1   514 1   A38668   IMP dehydrogenase
    13 1324.5   50.6   499 1   T32709   IMP dehydrogenase
    14   1155   44.1   502 2   F86298   IMP dehydrogenase
    15 1106.5   42.2   503 1   JC4999   IMP dehydrogenase
    16 1043.5   39.8   403 2   S53477   IMP dehydrogenase
    17   966.5   36.9   485 2   G81308   IMP dehydrogenase
    18   958   36.6   485 2   D97232   IMP dehydrogenase
```

RESULT 1
A31997
IMP dehydrogenase (EC 1.1.1.205) II - human
N;Alternate names: inosine 5'-monophosphate dehydrogenase (IMPDH) type II
C;Species: Homo sapiens (man)
C;Date: 21-May-1990 #sequence_revision 22-May-1998 #text_change 09-Jul-2004
C;Accession: I52303; I54184; A92676; B35566; A31997; A94550
R;Glesne, D.A.; Huberman, E.
Biochem. Biophys. Res. Commun. 205, 537-544, 1994
A;Title: Cloning and sequence of the human type II IMP dehydrogenase gene.
A;Reference number: I52303; MUID:95091778; PMID:7999076
A;Accession: I52303
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-514 <GLE1>
A;Cross-references: UNIPROT:P12268; GB:L33842; NID:g602457; PIDN:AAA67054.1;
PID:g602458
R;Glesne, D.A.; Collart, F.R.; Varkony, T.; Drabkin, H.; Huberman, E.
Genomics 16, 274-277, 1993
A;Title: Chromosomal localization and structure of the human type II IMP
dehydrogenase gene.
A;Reference number: I54184; MUID:93252398; PMID:8098009
A;Accession: I54184
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 461-514 <GLE2>
A;Cross-references: GB:L08114; NID:g292239; PIDN:AAA36113.1; PID:g292240
R;Collart, F.R.; Huberman, E.
J. Biol. Chem. 263, 15769-15772, 1988
A;Title: Cloning and sequence analysis of the human and Chinese hamster inosine-
5'-monophosphate dehydrogenase cDNAs.
A;Reference number: A92676; MUID:89008491; PMID:2902093
A;Accession: A92676
A;Molecule type: mRNA
A;Residues: 1-189,'RS',192-514 <COL>
A;Cross-references: GB:J04208; NID:g186391; PIDN:AAA36112.1; PID:g307066
A;Note: submitted to the Protein Sequence Database, November 1989
R;Natsumeda, Y.; Ohno, S.; Kawasaki, H.; Konno, Y.; Weber, G.; Suzuki, K.
J. Biol. Chem. 265, 5292-5295, 1990
A;Title: Two distinct cDNAs for human IMP dehydrogenase.
A;Reference number: A35566; MUID:90203022; PMID:1969416
A;Accession: B35566
A;Status: nucleic acid sequence not shown; not compared with conceptual
translation
A;Molecule type: mRNA
A;Residues: 1-514 <NAT>
C;Comment: mRNA for IMP dehydrogenase I (see PIR:A35566) predominated in normal
leukocytes, whereas that for IMP dehydrogenase II predominated in ovarian tumor
cells.
C;Genetics:
A;Gene: GDB:IMPDH2
A;Cross-references: GDB:128086; OMIM:146691
A;Map position: 3p24.2-3p21.2
A;Introns: 33/2; 49/3; 83/3; 108/3; 177/3; 207/1; 274/1; 304/1; 336/1; 432/2;
480/2; 508/2
C;Function:

A;Description: catalyzes the oxidation of inosine 5'-phosphate by NAD and one molecule of water to xanthosine 5'-phosphate
A;Pathway: purine nucleotide biosynthesis
C;Superfamily: inosine-5'-monophosphate dehydrogenase; CBS homology; IMP dehydrogenase amino-terminal homology; IMP dehydrogenase catalytic homology
C;Keywords: GMP biosynthesis; NAD; oxidoreductase; purine nucleotide biosynthesis
F;30-96/Domain: IMP dehydrogenase amino-terminal homology <IDHN>
F;117-168/Domain: CBS homology <CBS1>
F;184-232/Domain: CBS homology <CBS2>
F;233-476/Domain: IMP dehydrogenase catalytic homology <IDHC>
F;331/Active site: Cys #status predicted

```
    Query Match               99.1%;   Score 2595;   DB 1;   Length 514;
    Best Local Similarity     99.2%;   Pred. No. 8.7e-159;
    Matches  510;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy         1 MADYLISGGTSYVPDDGLTAQQLFNCGDGLTYNDFLILPGYIDFTADQVDLTSALTKKIT 60
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1 MADYLISGGTSYVPDDGLTAQQLFNCGDGLTYNDFLILPGYIDFTADQVDLTSALTKKIT 60

Qy        61 LKTPLVSSPMDTVTEAGMAIAMALTGGIGFIHHNCTPEFQANEVRKVKKYEQGFITDPVV 120
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        61 LKTPLVSSPMDTVTEAGMAIAMALTGGIGFIHHNCTPEFQANEVRKVKKYEQGFITDPVV 120

Qy       121 LSPKDRVRDVFEAKARHGFCGIPITDTGRMGSRLVGIISSRDIDFLKEEEHDCFLEEIMT 180
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       121 LSPKDRVRDVFEAKARHGFCGIPITDTGRMGSRLVGIISSRDIDFLKEEEHDCFLEEIMT 180

Qy       181 KREDLVVAPRSITLKEANEILQRSKKGKLPIVNEDDELVAIIARTDLKKNRDYPLASKDA 240
             |||||||||   |||||||||||||||||||||||||||||||||||||||||||||||
Db       181 KREDLVVAPAGITLKEANEILQRSKKGKLPIVNEDDELVAIIARTDLKKNRDYPLASKDA 240

Qy       241 KKQLLCGAAIGTHEDDKYRLDLLAQAGVDVVVLDSSQGNSIFQINMIKYIKDKYPNLQVI 300
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       241 KKQLLCGAAIGTHEDDKYRLDLLAQAGVDVVVLDSSQGNSIFQINMIKYIKDKYPNLQVI 300

Qy       301 GGNVVTAAQAKNLIDAGVDALRVGMGSGSICIIQEVLACGRPQATAVYKVYEYARRFGVP 360
             |||||||||||||||||||||||||||||| ||||||||||||||| |||||||||
Db       301 GGNVVTAAQAKNLIDAGVDALRVGMGSGSICITQEVLACGRPQATAVYKVSEYARRFGVP 360

Qy       361 VIADGGIQNVGHIAKALALGASTVMMGSLLAATTEAPGEYFFSDGIRLKKYRGMGSLDAM 420
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       361 VIADGGIQNVGHIAKALALGASTVMMGSLLAATTEAPGEYFFSDGIRLKKYRGMGSLDAM 420

Qy       421 DKHLSSQNRYFSEADKIKVAQGVSGAVQDKGSIHKFVPYLIAGIQHSCQDIGAKSLTQVR 480
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       421 DKHLSSQNRYFSEADKIKVAQGVSGAVQDKGSIHKFVPYLIAGIQHSCQDIGAKSLTQVR 480

Qy       481 AMMYSGELKFEKRTSSAQVEGGVHSLHSYEKRLF 514
             ||||||||||||||||||||||||||||||||||
Db       481 AMMYSGELKFEKRTSSAQVEGGVHSLHSYEKRLF 514
```

```
Database :          UniProt_03:*
                    1:  uniprot_sprot:*
                    2:  uniprot_trembl:*

         Pred. No. is the number of results predicted by chance to have a
         score greater than or equal to the score of the result being printed,
         and is derived by analysis of the total score distribution.


                                        SUMMARIES
                      %
Result              Query
   No.    Score   Match Length DB   ID                        Description
       ------------------------------------------------------------------------------
       1    2595    99.1    514  1   IMD2_HUMAN                P12268 homo sapien
       2    2561    97.8    514  1   IMD2_MOUSE                P24547 mus musculu
       3    2559    97.7    514  1   IMD2_CRIGR                P12269 cricetulus
       4    2547    97.3    514  2   Q6P9U9                    Q6p9u9 rattus norv
       5    2422    92.5    514  2   Q66JD5                    Q66jd5 xenopus tro
       6    2411    92.1    514  2   Q7ZYP7                    Q7zyp7 xenopus lae
       7    2404    91.8    514  2   Q7ZXT8                    Q7zxt8 xenopus lae
       8    2395    91.4    514  2   Q7ZYW9                    Q7zyw9 brachydanio
       9    2256    86.1    514  2   Q7ZWN1                    Q7zwn1 xenopus lae
      10    2253    86.0    544  2   Q6GMG5                    Q6gmg5 brachydanio
      11    2234    85.3    514  1   IMD1_HUMAN                P20839 homo sapien
      12    2222    84.8    514  2   Q7TSG7                    Q7tsg7 mus musculu
      13    2203    84.1    514  1   IMD1_MOUSE                P50096 mus musculu
      14  2093.5    79.9    530  2   Q6ZNB1                    Q6znb1 homo sapien
      15  1830.5    69.9    559  2   Q7QHD0                    Q7qhd0 anopheles g
      16  1764.5    67.4    537  1   IMDH_DROME                Q07152 drosophila
      17  1614.5    61.6    522  2   Q756Z6                    Q756z6 ashbya goss
      18  1610.5    61.5    524  1   IMD4_YEAST                P50094 saccharomyc
      19  1608.5    61.4    526  2   Q6C897                    Q6c897 yarrowia li
      20  1607.5    61.4    523  1   IMD3_YEAST                P50095 saccharomyc
      21  1605.5    61.3    521  1   IMH3_CANAL                O00086 candida alb
      22  1597.5    61.0    521  2   Q9P8J2                    Q9p8j2 candida alb
```